

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 9, 2003, 16:23:48 ; Search time 48.0429 Seconds
(without alignments)
102.055 Million cell updates/sec

Title: US-09-905-691-2

Perfect score: 19

Sequence: 1 ARAARRAARRAARRA 19

Scoring table: OLIGO 60.0, Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size: 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	52.6	406	10 Q94EV7	Q94ev7 zea mays (m
2	9	47.4	105	2 P96802	P96802 mycobacteri
3	9	47.4	105	16 Q9CCQ8	Q9CCQ8 mycobacteri
4	9	47.4	190	16 P71658	P71658 mycobacteri
5	9	47.4	750	16 Q9KXP6	Q9KXP6 streptomyc
6	8	42.1	101	11 Q8BMV6	Q8BMV6 mus musculu
7	8	42.1	127	2 Q8G161	Q8G161 terrabacter
8	8	42.1	144	17 Q9YD73	Q9YD73 aeropyrum p
9	8	42.1	167	10 Q8SLJ9	Q8SLJ9 oryza sativ
10	8	42.1	200	2 Q9X696	Q9X696 streptomyc
11	8	42.1	204	12 Q65545	Q65545 bovine herp
12	8	42.1	274	10 Q8GZE4	Q8GZE4 pyrocystis
13	8	42.1	327	2 Q30370	Q30370 pseudomonas
14	8	42.1	338	16 Q91LL5	Q91LL5 pseudomonas
15	8	42.1	336	2 Q9X4X0	Q9X4X0 pseudomonas
16	8	42.1	356	7 Q31191	Q31191 mus musculu

ALIGNMENTS

RESULT 1

Q94EV7	PRELIMINARY;	PRT;	406 AA.
ID Q94EV7			
AC Q94EV7	01-DEC-2001 (TRENBLrel. 19, Created)		
DT 01-DEC-2001	(TRENBLrel. 19, Last sequence update)		
DT 01-MAR-2003	(TRENBLrel. 23, Last annotation update)		
DE MAP kinase kinase			
GN MAPKK1			
OS Zea mays (Maize)			
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC PACCAD clade; Panicoideae; Andropogoneae; Zea			
OX NCBI_TaxID=4577;			
LN [1]			
RP SEQUENCE FROM N.A.			
RC TRANSPOSON-HUCK1			
RA Fu H., Zheng Z., Dooner H.K.;			
RT "Large differences in recombination rates within adjacent gene-dense			
RT and retrotransposon regions of maize."			
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.			
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
DR EMBL: AF391808; AAK73104.1;			
DR InterPro; IPR000719; Prot_kinase.			
DR InterPro; IPR002965; P_Rich_extensn.			
DR InterPro; IPR002290; Ser_thr_kinase.			
DR Pfam; PF00069; kinase; 1.			
DR PRINTS; PR01217; PRICHEXTENS.			
DR PRINTS; PR00109; TYRKINASE.			
DR PRODOM; PD000001; Prot_kinase; 1.			
DR SMART; SM00220; S_TKc; 1.			
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.			
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.			
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.			
SQ SEQUENCE 406 AA; 44664 MW; DBF1DE6568F47DFO CRC64;			

Query Match

52.6%; Score 10; DB 10; Length 406;

Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ARAARRAAAR 13
| | | | | | | |
DB 71 ARAARRAAAR 80

RESULT 2

P96802 ID P96802 PRELIMINARY; PRT; 105 AA.
AC P96802;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Integration host factor.
GN MIHF.
OS Mycobacterium smegmatis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;
RN [1]
RP SEQUENCE FROM N.A.
RA Pedulla M.L., Lee M.H., Lever D.C., Hatfull G.F.;
RT "A novel host factor for integration of mycobacteriophage L5.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
SQ EMBL; U75344; AAC28246.1; -;
SQ SEQUENCE 105 AA; 11635 MW; B73846DBFA6CA838 CRC64;

Query Match 47.4%; Score 9; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AARRARRAE 18
| | | | | | | |
DB 19 AARRARRAE 27

RESULT 3

Q9CC08 ID Q9CC08 PRELIMINARY; PRT; 105 AA.
AC Q9CC08;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE Putative integration host factor.
GN MIHF OR ML0540.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eigmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy I., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
DR EMBL; AL583918; CAC30048.1; -;
DR Leproma; ML0540; -;
KW Complete proteome.
SQ SEQUENCE 105 AA; 11506 MW; BDCD218AEFF76238 CRC64;

Query Match 47.4%; Score 9; DB 16; Length 105;

Best Local Similarity 100.0%; Pred. No. 3.1;

QY 10 AARRARRAE 18
| | | | | | | |
DB 104 AARRARRAE 112

RESULT 5

Q9KXP6 ID Q9KXP6 PRELIMINARY; PRT; 750 AA.
AC Q9KXP6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein SC01504.
GN SC01504 OR SC95.28.
OS Streptomyces coelicolor.

Query Match 47.4%; Score 9; DB 16; Length 105;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AARRARRAE 18
| | | | | | | |
DB 19 AARRARRAE 27

RESULT 4

P71658 ID P71658 PRELIMINARY; PRT; 190 AA.
AC P71658;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Hypothetical protein Rv1388.
GN Rv1388 OR MT1433 OR WCY21B4.05.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekaia F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy I.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares R., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: STRONG, TO M.SMEGMATIS MHF.
DR EMBL; Z80108; CAB02193.1; -;
DR EMBL; AS007015; AAK45698.1; ALT_INIT.
DR TIGR; MT1433; -;
DR Tuberculist; Rv1388; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 190 AA; 20835 MW; 376672DCF96AF60D CRC64;

Query Match 47.4%; Score 9; DB 16; Length 190;

Best Local Similarity 100.0%; Pred. No. 5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AARRARRAE 18
| | | | | | | |
DB 104 AARRARRAE 112

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OX Streptomycineae; Streptomycetaceae; Streptomycetes.

(1)

RP NCBI_TaxID=1902;

RC SEQUENCE FROM N.A.

RA STRAIN-A3(2);

RL Brown S.P., Harris D.,

RP Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

(2)

RP SEQUENCE FROM N.A.

RA STRAIN-A3(2);

RL Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.,

RP Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

(3)

RP SEQUENCE FROM N.A.

RA STRAIN-A3(2);

RL Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,

RP Kinashi H., Hopwood D.A.;

RA "A set of ordered cosmids and a detailed genetic and physical map for

RP the 8 Mb streptomycetes coelicolor A3(2) chromosome.";

(4)

RP SEQUENCE FROM N.A.

RA STRAIN-A3(2) / M145;

RL MEDLINE=21996410; PubMed=8843436;

RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

RP Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

RP Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,

RP Rabinovitch E., Rajandream M.A., Rutherford K., Rutter S.,

RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

RP Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,

RA Hopwood D.A.;

RP "Complete genome sequence of the model actinomycete Streptomycetes

RP coelicolor A3(2).";

RL Nature 417:141-147(2002).

DR EMBL; AL393109; CAB93384.1;

DR InterPro; IPR000767; Disease_resist.

DR PRINTS; PR00364; DISEASERIST.

KW Hypothetical protein; Complete proteome.

RP SEQUENCE 750 AA; 81839 MW; 469E5F417EDC8862 CRC64;

QY

Db

7 ARAAARRA 15

|||||

76 ARAAARRA 84

PRELIMINARY; PRT; 101 AA.

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Query Match 47.4%; Score 9; DB 15; Length 750;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

Db

7 ARAAARRA 15

|||||

76 ARAAARRA 84

PRELIMINARY; PRT; 101 AA.

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

Q8BMV6

RT

RL

DR

KW

FT

SO

SEQUENCE

101 AA;

10110 MW;

CBDCC2D530ABB15 CRC64;

Query Match

42.1%;

Score 8;

DB 11;

Length 101;

Best Local Similarity

100.0%;

Pred. No. 17;

Matches

8;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

QY

Db

6 RAARAAAR 13

|||||

67 RAARAAAR 74

PRELIMINARY; PRT; 127 AA.

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

60,770 full-length cDNAs.;

Nature 420:563-573(2002).

DR EMBL; AK021392; BAC25654.1;

KW Hypothetical protein.

FT NON_TER

SEQUENCE

101 AA;

10110 MW;

CBDCC2D530ABB15 CRC64;

Query Match

42.1%;

Score 8;

DB 11;

Length 101;

Best Local Similarity

100.0%;

Pred. No. 17;

Matches

8;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

QY

Db

6 RAARAAAR 13

|||||

67 RAARAAAR 74

PRELIMINARY; PRT; 127 AA.

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

Q8GI61

60,770 full-length cDNAs.;

Nature 420:563-573(2002).

DR EMBL; AK021392; BAC25654.1;

KW Hypothetical protein.

FT NON_TER

SEQUENCE

101 AA;

10110 MW;

CBDCC2D530ABB15 CRC64;

Query Match

42.1%;

Score 8;

DB 11;

Length 101;

Best Local Similarity

100.0%;

Pred. No. 17;

Matches

8;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

QY

Db

RL DNA Res. 6:83-101(1999).
 DR EMBL; AP000060; BAA80024.1;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 144 AA; 14937 MW; 973D6C61A0449375 CRC64;
 Query Match 42.1%; Score 8; DB 17; Length 144;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 AARAAARA 10
 Db | | | | | | | |
 3 AARAAARA 10
 RESULT 9
 Q8SLJ9 PRELIMINARY; PRT; 167 AA.
 AC Q8SLJ9
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE P0684C02.19 protein.
 GN P0684C02.19
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC
 clone: P0684C02.19".
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003290; BAB89063.1;
 DR Gramene; Q8SLJ9;
 SQ SEQUENCE 167 AA; 18542 MW; 0C40040DFB49021B CRC64;
 Query Match 42.1%; Score 8; DB 10; Length 167;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 RRAARAAA 12
 Db | | | | | | | |
 20 RRAARAAA 27
 RESULT 10
 Q9X696 PRELIMINARY; PRT; 200 AA.
 AC Q9X696
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE VdCB.
 GN VdCB.
 OS Streptomyces sp. (strain D7).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=92742;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D7;
 RA MEDLINE=99445180; PubMed=10517592;
 RX Chow K.T., Pope M.K., Davies J.;
 RT "Characterization of a vanillic acid non-oxidative decarboxylation
 gene cluster from Streptomyces sp. D7".
 RL Microbiology 145:2393-2403(1999).
 DR EMBL; AF134589; AAD28781.1;
 DR InterPro; IPR003382; Flavoprotein.
 DR InterPro; IPR004507; Ubix.
 DR Pfam; PF02441; Flavoprotein; 1.

DR TIGRFAMs; TIGR00421; ubiX; 1.
 SQ SEQUENCE 200 AA; 21660 MW; 83D1B5C32C13CD3E CRC64;
 Query Match 42.1%; Score 8; DB 2; Length 200;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 RAARAAAR 13
 Db | | | | | | | |
 187 RAARAAAR 194
 RESULT 11
 Q65545 PRELIMINARY; PRT; 204 AA.
 AC Q65545
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE UL3 protein.
 GN UL3
 OS Bovine herpesvirus 1.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.
 OX NCBI_TaxID=10320;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cooper;
 RX MEDLINE=96036477; PubMed=7483276;
 RA Khattar S.K., van Drunen Littel-van den Hurk S., Babiuk L.A.,
 RA Tikoo S.K.;
 RT "Identification and transcriptional analysis of a 3'-coterminial gene
 cluster containing UL1, UL2, UL3, and UL3.5 open reading frames of
 bovine herpesvirus-1".
 RL Virology 213:28-37(1995).
 DR EMBL; U32173; AAC54557.1;
 DR InterPro; IPR005035; Herpes_UL3.
 DR InterPro; IPR005829; Sug. transporter.
 DR Pfam; PF03369; Herpes_UL3_1.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1;
 SQ SEQUENCE 204 AA; 21792 MW; 9292E6A9AA3CB8C6 CRC64;
 Query Match 42.1%; Score 8; DB 12; Length 204;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 RAARAAAR 13
 Db | | | | | | | |
 113 RAARAAAR 120
 RESULT 12
 Q8GZE4 PRELIMINARY; PRT; 274 AA.
 AC Q8GZE4
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Chlorophyll A-C binding protein.
 OS Pyrocystis lunula.
 OC Eukaryota; Alveolata; Dinophyceae; Pyrocystales; Pyrocystis.
 OX NCBI_TaxID=2972;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Okamoto O.K., Hastings J.W.;
 RT "Circadian oscillations in the transcriptome of dinoflagellate cells:
 towards the clock circuitry".
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF508261; AAO14680.1;
 SQ SEQUENCE 274 AA; 28168 MW; B5F522A5D45AC8BA CRC64;
 Query Match 42.1%; Score 8; DB 10; Length 274;
 Best Local Similarity 100.0%; Pred. No. 39;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AAARRARA 17
| | | | | | | |
DB 81 AAARRARA 88

RESULT 13

ID Q30370 PRELIMINARY; PRT; 327 AA.
AC Q30370;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PVCA.
GN PVCA.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RX MEDLINE=96254009; PubMed=8704959;
RA Stintzi A., Cornelis P., Hohnadel D., Meyer J.M., Dean C., Poole K.,
RA Kourambas S., Krishnapillai V.,
RT "Novel pyoverdine biosynthesis gene(s) of Pseudomonas aeruginosa
RT PAO.";
RL Microbiology 142:1181-1190(1996).
[2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RX MEDLINE=99315810; PubMed=10383985;
RA Stintzi A., Johnson Z., Stonehouse M., Ochsaner U., Meyer J.M.,
RA Vasil M.L., Poole K.;
RT "The pvc gene cluster of Pseudomonas aeruginosa: role in synthesis of
RT the pyoverdine chromophore and regulation by PtxR and pvdS";
RL J. Bacteriol. 181:4118-4124(1999).
DR EMBL; AF002222; AAC21671.1;
SQ SEQUENCE 327 AA; 37019 MW; 08286F3B127C9B8B CRC64;

Query Match 42.1%; Score 8; DB 2; Length 327;

Best Local Similarity 100.0%; Pred. No. 45;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAARRARA 8
| | | | | | | |
DB 318 AAARRARA 325

RESULT 14

ID Q911L5 PRELIMINARY; PRT; 328 AA.
AC Q911L5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Pyoverdine biosynthesis protein PVCA.
GN PVCA OR PA2254.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004651; AAG05642.1;
KW Complete proteome.
SQ SEQUENCE 328 AA; 37134 MW; DE646CA9BEF43B29 CRC64;

Query Match 42.1%; Score 8; DB 16; Length 328;
Best Local Similarity 100.0%; Pred. No. 45;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAARRARA 8
| | | | | | | |
DB 319 AAARRARA 326

RESULT 15

ID Q9X4X0 PRELIMINARY; PRT; 336 AA.
AC Q9X4X0;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE DITH.
GN DITH.
OS Pseudomonas abietaniphila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=89065;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=BKME-9;
RA Mohn W.W., Wilson A.E., Bicho P., Moore E.R.B.;
RT "Physiological and Phylogenetic Diversity of Bacteria Growing on Resin
RT Acids.";
RL Syst. Appl. Microbiol. 0:0-0(1999).
[2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=BKME-9;
RX MEDLINE=99235742; PubMed=10217753;
RA Martin V.J., Mohn W.W.;
RT "A novel aromatic-ring-hydroxylating dioxygenase from the diterpenoid-
RT degrading bacterium Pseudomonas abietaniphila BKME-9.";
RL J. Bacteriol. 181:2675-2682(1999).
DR EMBL; AF119621; AAD21070.1;
DR InterPro; IPR002529; FAA_Hydrolase.
DR Pfam; PF01557; FAA_Hydrolase; 1.
SQ SEQUENCE 336 AA; 37494 MW; CD221163F81B44FB CRC64;

Query Match 42.1%; Score 8; DB 2; Length 336;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AAARRARA 17
| | | | | | | |
DB 105 AAARRARA 112

Search completed: August 9, 2003, 16:32:55
Job time : 51.0429 secs